QP501.J7

STIC-ILL

From: Steadman, David (AU1652)
Sent: Thursday, April 19, 2001 7:31 AM
To: STIC-ILL
Subject: Literature/ILL Request

Art Unit: 1652
Room #: 8B-11
Mailbox #: 10C-01 M3
Serial #: 09/520,538

Please provide the following references:

1) J. Biol. Chem., Vol. 269, Issue 11, 8059-8062, Mar, 1994
Genetic evidence for activation of the positive transcriptional regulator Xy1R, a member of the NtrC family of regulators, by effector binding
A Delgado and JL Ramos

2) J Bacteriol 1992 Feb;174(3):711-24
Nucleotide sequence and functional analysis of the complete phenol/3,4-dimethylphenol catabolic pathway of Pseudomonas sp. strain CF600.
Shingler V, Powlowski J, Marklund U.

Thank you,
David Steadman

THE JOURNAL OF BIOLOGICAL CHEMISTRY
Vol. 269, No. 11, Issue of March 18, pp. 8059-8062, 1994
Printed in U.S.A.

Genetic Evidence for Activation of the Positive Transcriptional Regulator XylR, a Member of the NtrC Family of Regulators, by Effector Binding*

(Received for publication, October 5, 1993, and in revised form, December 1, 1993)

Asunción Delgado‡ and Juan-Luis Ramos§

From the Consejo Superior de Investigaciones Cientificas-Estación Experimental del Zaidín, Department of Plant Biochemistry, Apdo Correos 419, E-18008 Granada, Spain

The XylR protein positively controls expression from the *Pseudomonas putida* TOL plasmid σ^{54}-dependent Pu and Ps promoters, in response to the presence of aromatic effectors such as *m*-xylene, *m*-methylbenzyl alcohol, and *p*-chlorobenzaldehyde in the culture medium. XylR also autoregulates its own synthesis. A mutant XylR regulator called XylR7 was isolated after nitrosoguanidine mutagenesis of the wild-type gene and phenotypic selection for mutants that had acquired the ability to recognize *m*-nitrotoluene, a nitroarene that is not an effector for the wild-type regulator. The mutant regulator exhibited a single point mutation that resulted in a change in codon 172 (GAA → AAA), which should result in a Glu → Lys change in the polypeptide chain. The effector profile of the mutant regulator was determined by measuring β-galactosidase from a fusion of the Pu promoter to a promoterless *lacZ* gene. The results showed that the mutant regulator had acquired the ability to recognize *m*-nitrotoluene, and retained the wild-type regulator's ability to recognize most of the wild-type effectors. Full transcriptional activation of the Pu promoter by XylR7, as with the wild-type XylR protein, requires its full modular structure, namely the σ^{54} recognition site, the integration host factor binding site, and the upstream activation sequences. The XylR7 regulator did not stimulate transcription from the Ps promoter in response to the presence of its effectors, and autoregulated its own synthesis at low levels.

The TOL plasmid pWW0 of *Pseudomonas putida* encodes the genetic information for the mineralization of toluene and xylenes via benzoate and toluates (1). The genes of the catabolic pathways are organized in four transcriptional units. Two of these, the "upper" and the *meta* pathway operons, contain the *xyl* structural genes encoding the corresponding catabolic enzymes for the oxidation of toluene/xylenes via benzoate/toluates to amphibolic intermediates, whereas the two remaining genes, *xylR* and *xylS*, encode regulatory proteins. Fig. 1 summarizes the transcriptional loops in cells growing on aromatic hydrocarbons.

* This work was supported in part by a grant from the Comisión Interministerial de Ciencia y Tecnología of Spain (CICYT BIO91-0659) and a grant from the European Commission (CE-BRIDGE-CT-91-0293). The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "*advertisement*" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

‡ Recipient of a predoctoral fellowship.

§ To whom all correspondence should be addressed: Estación Experimental del Zaidín, Apdo Correos 419, E-18008 Granada, Spain. Tel.: 34-58-121011; Fax: 34-58-129600.

The XylR protein is the ultimate regulator involved in the transcriptional activation of the TOL catabolic pathways. The *xylR* gene is constitutively transcribed from two tandem promoters (2), but the XylR protein only stimulates transcription from its cognate regulated promoters, the upper pathway operon Pu, and the *xylS* gene promoter Ps, in response to the presence of a series of aromatics such as *m*-xylene, *m*-methylbenzyl alcohol, and *p*-chlorobenzaldehyde (3). Activation of transcription from Ps triggers a cascade system, the hyperproduction of the XylS protein in turn stimulating transcription from the *meta*-cleavage pathway operon to obtain the breakdown of the aromatics to amphibolic intermediates (4, 5).

The XylR-activated promoters on the *P. putida* TOL plasmid Ps and Pu belong to the −12/−24 family, and are dependent on the RpoN σ-factor (also called NtrA and σ^{54}). In addition, transcription from Pu but not from Ps is also dependent on IHF[1] (6, 7). As is the case with other σ^{54}-dependent promoters (8, 9), upstream activation sequences (UASs) located between 120 and 180 base pairs from the main transcription initiation point are necessary for XylR-mediated induction by toluene, xylenes, and other pathway substrates (6, 7, 10). Close proximity between the upstream bound activator and the promoter site is believed to be brought about by DNA loop formation, which is apparently aided in the case of the Pu promoter by the binding of the IHF protein at a site between the promoter and upstream activator sequence (6, 7).

The XylR protein shows significant sequence similarities with NtrC and other members of this family of regulators (11, 12). In the case of NtrC and other members of the family, activation of the regulator involves its phosphorylation mediated by a protein kinase that functions as the sensory element (13). The XylR regulator, both in *P. putida* and when cloned in *Escherichia coli*, activates transcription from Pu and Ps promoters in response to effectors. This has been taken as evidence of the activation of the regulator after effector binding. In this article we show that a mutant XylR exhibiting a single amino acid change at the N-terminal end acquires the ability to recognize *m*-nitrotoluene, which is not an effector for the wild-type protein.

EXPERIMENTAL PROCEDURES

Bacterial Strains, Plasmids, and Growth Conditions—Bacterial strains used in this work were *E. coli* MC4100 (F⁻, *ara*D139, Δ[*argF-lac*U169], *rps*L150, *rel*A, *flb*5301, *pts*F25, *deo*C1), *E. coli* ET8000 (*rbs*, *lac*Z::IS1, *gyr*A, *hut*C⁻), and *E. coli* ET8045 (ET8000 [*ntr*A::Tn10],Tet^r).

Plasmids used were pTS174 (Cm^r, *xylR*⁺, P15 replicon) (14), pAD1 (Cm^r, *xylR7*, P15 replicon) (this study), pRD579 (Ap^r, Pu::*lacZ*, pR1 replicon) (15), pAH100 (Ap^r, Ps::*lacZ*, pR1 replicon) (16), pAH120 (Ap^r Pr::*lacZ*, pR1 replicon) (16), pTZ19 (Ap^r, cloning and sequencing vector)

[1] The abbreviations used are: IHF, integration host factor; UAS, upstream activation sequence.

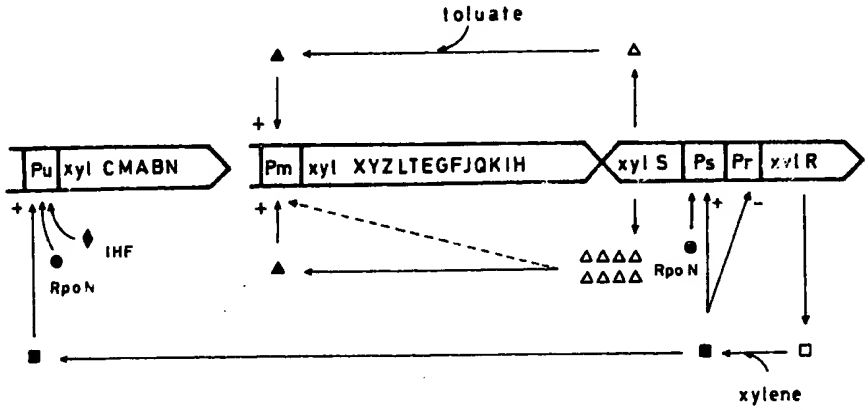

FIG. 1. **Transcriptional loops in the control of the TOL catabolic pathways for the metabolism of aromatic hydrocarbons.** For details and genetic organization of the upper operon (*xyl*CMABN), the *meta* operon (*xyl*XYZ...H), and regulatory genes *xyl*S and *xyl*R, see Harayama and Timmis (40). □, XylRi, a XylR form unable (or only able inefficiently) to stimulate transcription from Pu and Ps; ■, XylRa, an active XylR form that, with RpoN (●), stimulates transcription from Ps, and with RpoN and IHF (♦) stimulates transcription from Pu. XylR by itself autoregulates its own synthesis; △, XylSi, a XylS form that at low concentration does not stimulate transcription from Pm; ▲, XylSa, an active XylS form that stimulates transcription from Pm. +, stimulation of transcription; −, inhibition of transcription.

(17), pERD401 (Ap^r, Pu::*lacZ*, pBR replicon) (6), and pERD412 (Ap^r, ΔPu::*lacZ*, pBR replicon) (18).

Bacteria were grown at 30 °C in LB broth supplemented when required with 100 μg/ml ampicillin and 30 μg/ml chloramphenicol.

xylR Mutants—E. coli MC4100 bearing pTS174 was grown at 30 °C until the culture reached a cell density of about 0.6 at 660 nm. One ml of cells was removed and incubated for 10 min at 30 °C with *N'*-methyl-*N'*-nitro-*N*-nitrosoguanidine (30 μg/ml). Cells were washed, resuspended in 2 ml of LB and incubated for 3 h at 37 °C. Plasmid DNA was then extracted from the cells surviving mutagenesis, and used to transform MC4100 (pRD579). Ampicillin- and chloramphenicol-resistant colonies were selected on McConkey plates exposed to *m*-nitrotoluene vapors. Red papillaceae colonies were chosen, purified, and used to test the response to *m*-nitrotoluene in liquid culture medium. To further confirm that in positive clones the character was associated to XylR, the Cm^r pTS174 derivative from these clones was isolated and transformed in *E. coli* ET8000 (pRD579), and β-galactosidase expression in response to *m*-nitrotoluene was again measured. One such mutant responded to *m*-nitrotoluene in this host and was kept for further studies. The mutant plasmid was called pAD1 and the mutant *xyl*R gene was called *xyl*R7.

β-Galactosidase Assays—E. coli ET8000 cells carrying pRD579 plus a compatible plasmid bearing the wild-type *xyl*R allele (pTS174) or the *xyl*R7 allele (pAD1) were grown overnight on LB medium containing the appropriate antibiotics. The cells were diluted 1:100 in the same medium and incubated for 2 h at 30 °C with shaking to allow cells to enter the logarithmic phase. At this time the medium was supplemented or not with 1 mM of an effector dissolved in dimethylformamide, and after 5 h of incubation (A_{650} = 3.0–4.0) β-galactosidase was assayed in permeabilized cells as described previously (19). β-Galactosidase activity was expressed in Miller's units.

The expression from Ps and Pr fused to a promoterless *lacZ* gene was determined as described by Holtel *et al.* (16) in *E. coli* ET8000 bearing pAH100 and pAH120 with and without XylR or XylR7, in the presence and absence of effectors.

DNA Techniques—DNA isolation, analysis by agarose gel electrophoresis, digestion with restriction enzymes, and transformations were done according to standard procedures or the manufacture's recommendations. DNA was sequenced by the dideoxy chain termination method using ^{35}S-labeled nucleotide, a series of *xyl*R-specific 20-mer oligonucleotides to prime synthesis, and 7-deaza-dGTP instead of dGTP to eliminate compressions due to the high G + C content of the *xyl*R gene. The 5'-mRNA start of the upper operon transcript was determined by primer extension analysis as described previously (20). The oligonucleotide 5'-GATGTGCTGCAAGGCGATTAAGTTG-3' was 5'-end labeled with [γ-^{32}P]ATP and annealed to 20 μg of total RNA prepared from *E. coli* pERD401 (Pu::*lacZ* fusion) also bearing pTS174 (*xyl*R) or pAD1 (xylR7), grown in the absence and presence of *m*-nitrotoluene.

Sequence Analysis—Profile analysis of the XylR family was done using the FASTA program from the GCG sequence analysis package (21). Significance tests for similarities between members of the family were done using the Dayhoff M78 Matrix (22, 23) available in the PC-GENE package. Multiple alignments were done with the PILEUP program from the GCG package.

RESULTS

Sequence Changes of the xylR7 Mutant Allele

To identify the mutation(s) induced by nitrosoguanidine, the 2.5-kilobase *Hpa*I fragment of pAD1 carrying the mutant *xyl*R allele was sequenced in pTZ19. The entire nucleotide sequence of the *xyl*R allele from −170 to +1925 was determined using a series of *xyl*R-specific 20-mer oligonucleotides to prime synthesis. The sequence mutant allele exhibited a single base pair change at position 514 (G → A) from the first A of the ATG start codon. The G → A change in codon 172 (GAA → AAA) should result in an Glu → Lys change in the polypeptide chain.

Effector Profile of the Mutant Regulator XylR7

Stimulation of Transcription from the Upper Pathway Operon—The effector profile of the wild-type and the mutant XylR7 was determined by measuring β-galactosidase expression from a Pu::*lacZ* fusion in the low copy number plasmid pRD579. Plasmids pTS174 (*xyl*R) and pAD1 (*xyl*R7) were transformed in *E. coli* ET8000 (pRD579), and β-galactosidase activity in response to a number of aromatics was assayed. This strain was chosen because it gave the clearest induction results. Table I shows the effector profile of the wild-type regulator, which was similar to that reported by Abril *et al.* (3). The XylR protein exhibited a very broad spectrum of effectors, as it is able to recognize a wide variety of xylenes, *m*-methylbenzyl alcohol, *p*-chlorobenzaldehyde, and *o*- and *p*-nitrotoluene, but not *m*-nitrotoluene (Table I). The mutant XylR7 protein had acquired the ability to recognize *m*-nitrotoluene and retained the wild-type characteristic of recognizing and mediating high transcriptional levels with *o*- and *p*-nitrotoluene (see Table I). The XylR7 regulator also responded to *m*-xylene, *m*-methylbenzyl alcohol, and *p*-chlorobenzaldehyde (Table I). It should be mentioned that *o*-, *m*- and *p*-nitrobenzyl alcohol and *m*-nitrobenzaldehyde were not effectors for either the wild-type XylR or the XylR7 mutant regulators. The 5'-mRNA start point from the Pu promoter mediated by XylR7 and activated by *m*-nitrotoluene was, as expected, the same as that previously reported by Inouye *et al.* (24) for the wild-type regulator activated by *m*-xylene (not shown).

Abril and Ramos (18) have reported that the Pu promoter exhibits a modular structure that is required for full transcrip-

TABLE I
Effector profile of XylR and XylR7 as determined by using a Pu::lacZ fusion

E. coli ET8000 (pRD579) also bearing either pTS174 (*xylR*) or pAD1 (*xylR7*) were grown with vigorous shaking in the absence or presence of 1 mM of the above aromatics dissolved in dimethylformamide. Other experimental details are given under "Experimental Procedures." The data are the averages and the standard deviations of at least three independent determinations.

Effector	β-Galactosidase	
	XylR	XylR7
	units	
None	300 ± 15	150 ± 20
m-Xylene	1550 ± 240	500 ± 70
m-Methylbenzyl alcohol	1150 ± 170	450 ± 50
p-Chlorobenzaldehyde	1750 ± 250	720 ± 10
o-Nitrotoluene	1350 ± 220	1400 ± 300
m-Nitrotoluene	150 ± 30	950 ± 150
p-Nitrotoluene	1150 ± 150	850 ± 60

tional stimulation, namely, the σ^{54} recognition site, the IHF binding site, and the UASs. The requirement for σ^{54} (NtrA) and IHF for transcriptional stimulation from Pu by XylR7 was demonstrated using appropriate *E. coli* mutant strains and their isogenic parental strains. In fact, stimulation of transcription by XylR7 from the wild-type Pu promoter was not observed in the NtrA$^-$ strain *E. coli* ET8045, in contrast with full induction in ET8000 (Table II). As with the wild-type XylR regulator, induction from Pu with XylR7 and effectors in an IHF$^-$ background was about 10–25% of the level in the IHF$^+$ background. We also assayed activation by XylR and XylR7 from the wild-type Pu promoter in pERD401 and a mutant Pu derivative lacking the UAS1 region in pERD412. The mutant Pu promoter exhibited a deletion from −160 to −180 with respect to the main transcription initiation point (UAS1). With this mutant Pu promoter, no transcriptional activation in response to aromatic effectors was observed with either XylR or XylR7, suggesting that this UAS region is required for activation of transcription by XylR7 (not shown). Therefore, the mutation in the XylR regulator seems to affect primarily interactions with the effector, and requires the full modular structure of the Pu promoter to stimulate transcription.

Stimulation of Transcription from the xylS Gene Promoter by XylR and XylR7—To determine whether the mutant XylR7 regulator stimulated transcription from the Ps promoter, *E. coli* ET8000 bearing pAH100 (Ps::*lacZ*) was transformed with pTS174 and pAD1. We determined β-galactosidase activity in the absence and presence of 5 mM *m*-xylene, *m*-nitrotoluene, and *m*-methylbenzyl alcohol. The induction pattern from Ps by XylR was similar to that reported by Holtel *et al.* (16): β-galactosidase was observed in cells growing in the presence of *m*-xylene and *m*-methylbenzyl alcohol but not with *m*-nitrotoluene (Table III). Unexpectedly, XylR7 did not mediate activation of transcription from Ps in response to *m*-nitrotoluene or the other aromatics (Table III).

XylR7 Weakly Regulates Its Own Synthesis

The wild-type XylR protein autoregulates its own synthesis. The fusion pAH120 (Pr::*lacZ*) was used to study whether XylR7 also autoregulates its own synthesis; XylR was used as a control. As shown in Table IV, the transcriptional level from Pr in the presence of XylR with and without effector was reduced to about 40–50% of the level in the absence of the regulator. With the XylR7 regulator, the level of repression from the Pr promotor was only about 25% of the level in its absence. These results suggest that the XylR7 regulator showed an altered ability to regulate its own synthesis (Table IV).

TABLE II
Activation of the Pu promoter by XylR and XylR7 in different genetic backgrounds

The *E. coli* ET8000 and ET8045 were transformed with pRD579 (Pu::*lacZ*) and either pTS174 (*xylR*) or pAD1 (*xylR7*), and were grown in the presence or absence of 1 mM *m*-methylbenzyl alcohol (*m*-MBA) or *m*-nitrotoluene (*m*-NT). Other experimental details are given under "Experimental Procedures."

Strain	Relevant background	Effector	β-Galactosidase Pu::*lacZ*
ET8000	NtrA$^+$, XylR$^+$	None	300
		m-MBA	1700
		m-NT	200
ET8045	NtrA$^-$, XylR$^+$	None	20
		m-MBA	20
		m-NT	30
ET8000	NtrA$^+$, XylR7	None	150
		m-MBA	550
		m-NT	800
ET8045	NtrA$^-$, XylR7	None	30
		m-MBA	30
		m-NT	30

TABLE III
Activation of the Ps promoter by XylR and XylR7

E. coli ET8000 (pAH100) was transformed or not with pTS174 (*xylR*) and pAD1 (*xylR7*). Bacteria were grown for 16 h with vigorous shaking in the absence or presence of 5 mM *m*-xylene, *m*-methylbenzyl alcohol, and *m*-nitrotoluene. The data are the averages and standard deviations of at least three independent determinations. Other experimental details are given under "Experimental Procedures."

Effector	β-Galactosidase	
	XylR	XylR7
None	140 ± 20	140 ± 30
m-Xylene	360 ± 20	170 ± 20
m-Methylbenzyl alcohol	1000 ± 150	240 ± 35
m-Nitrotoluene	50 ± 10	150 ± 30

TABLE IV
Regulation of expression from Pr by XylR and XylR7

Conditions are as described in the legend to Table II except that *E. coli* bore pAH120 instead of pAH100. The data are the averages and standard deviations of at least three independent determinations. Number in parentheses are percentage of activity.

Effector	β-Galactosidase activity; regulator		
	None	XylR	XylR7
None	580 ± 50 (100)	260 ± 25 (46)	430 ± 30 (75)
m-Methylbenzyl alcohol	520 ± 40 (100)	200 ± 20 (39)	380 ± 40 (73)

DISCUSSION

The XylR protein, which stimulates transcription from the σ^{54}-dependent Pu and Ps promoters in the TOL plasmid pWW0 of *P. putida* (4, 25, 26), belongs to the NtrC family of regulators (12, 27). Within this family the greatest similarity, based on the algorithm of Needleman and Wunsch (22, 23), was to DmpR, the regulator for the phenol *meta*-cleavage pathway for phenol degradation by *P. putida* (28). The XylR protein also has a high similarity score with AlgB (29) and PilR (30) of *Pseudomonas aeruginosa*, DctD of *Rhizobium melilotti* (31), and FlbD of *Caulobacter crescentus* (32), among the members of the NtrC family. It should be noted that the similarity scores of XylR with NifA from *Klebsiella pneumoniae* (33), AnfA from *Azotobacter vinelandii* (34), and TyrR from *E. coli* (35) (members of the NtrC family) were not significant, which probably reflects evolutionary divergences within the family.

Multiple alignment of the protein sequences of the NtrC family revealed the greatest similarity extending to the central region (residues 234–472 in XylR; see Fig. 2) (27), which is

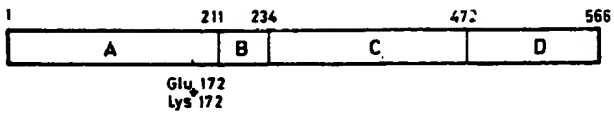

FIG. 2. **Modular structure of the XylR regulator.** The domains *A*, *B*, *C*, and *D* were established through multiple alignments of the highly homologous members of this family of regulators. *Numbers* indicate the boundaries of the domains in the XylR regulator, and $Glu^{172} \rightarrow$ Lys indicates the mutation in the XylR7 regulator.

probably involved in ATP hydrolysis, dimerization, and interaction with σ^{54} (27). The DNA binding motif at the C-terminal end, where a potential α-helix turn α-helix motif (residues 534–553 in XylR) was found, also seems to be conserved. The N-terminal region of XylR did not exhibit sequence conservation with the other members of the family, except for DmpR (28). This region has been proposed to be responsible for signal/sensor reception. In fact, the NtrC regulator, the prototype protein of this family, is activated by phosphorylation of an aspartyl residue at the N-terminal region by the kinase activity of NtrB, a protein that senses cellular N status (13, 36, 37). This mode of activation has been shown to work for the activation of other members of the family and other prokaryote transcriptional regulators, *e.g.* OmpR and NarL (38, 39). In contrast, activation of the XylR and DmpR regulators, which share 64% similarity at their N-terminal end, and are involved in the activation of catabolic pathways for metabolism of aromatics by *Pseudomonas*, seems to involve direct interaction of the effector and the regulator rather than phosphorylation. Evidence for this hypothesis arises from the following facts. (i) These regulators, when cloned in a host other than their natural host (*e.g. E. coli*) only promoted transcription from their cognate regulatable promoters in response to the presence of aromatic effectors (3, 28). (ii) In the case of XylR, the effector profile of the regulator has been studied in *P. putida*, its natural host, and *E. coli*; these studies included a number of aromatic hydrocarbons, benzyl alcohol, and benzaldehyde derivatives. The pattern of induction in *P. putida* and *E. coli* was similar, suggesting that the regulator response is specific (3). (iii) In this study we have shown that the substitution of Lys for Glu^{172} in the XylR regulator leads to a mutant regulator that acquires the ability to stimulate transcription in response to *m*-nitrotoluene, a character not present in the wild-type regulator. The fact that an alteration in the protein sequence leads to alterations in the profile effector suggests, but does not prove, that residue 172 is important for interaction(s) with the effector.

We found that stimulation of transcription from the Pu promoter by effector-activated XylR7 (as was also the case with the wild-type regulator) required the full modular structure of the Pu promoter. This suggests that the mechanism of XylR7 activation of transcription from the Pu promoter is similar to that of the wild-type regulator; therefore the main alteration in XylR7 seems to involve interactions with the effector. However, a surprising finding was that this mutant regulator was unable to promote transcription from Ps, and weakly autoregulated its own synthesis (Tables III and IV). These findings indicate that XylR7 may be affected in interactions with its target DNA sequences at the overlapping Ps/Pr promoters, which are similar but not identical to those in the Pu promoter. Differences in the activation of Pu and Ps has been noted before. (i) Full stimulation of transcription from Pu required IHF protein, whereas activation of the Ps promoter was IHF-independent (6, 7, 16), and (ii) stimulation of transcription by wild-type XylR activated by effectors from the Pu promoter was about 4-fold stronger than stimulation from the Ps promoter under all conditions tested.[2] Because the hydropatic profile of the region around residue 172 is altered due to the substitution of a lysine residue for a glutamyl residue, the alteration induced by this amino acid change may have been transmitted to other regions of the regulator in the three-dimensional structure of the regulator (*i.e.* the DNA binding domain), leading to subtle alterations in contacts with the corresponding UASs. Interactions at the Ps/Pr promoters may thus have been impeded, whereas this probably did not occur with the Pu promoter.

In summary, XylR is homologous to other regulators of the NtrC family, which includes proteins from different genera; however, it differs from the prototype protein of this family in that its interconversion between active and inactive forms is likely to be mediated by effector binding rather than by covalent modification catalyzed by a sensory protein.

Acknowledgments—We thank A. Holtel for plasmids and strains, M. T. Gallegos for support in computer analyses, and Silvia Marqués for help in primer extension.

REFERENCES

1. Worsey, M. J., and Williams, P. A. (1975) *J. Bacteriol.* **124,** 7–13
2. Inouye, S., Nakazawa, A., and Nakazawa, T. (1985) *J. Bacteriol.* **163,** 863–869
3. Abril, M. A., Michan, C., Timmis, K. N., and Ramos, J. L. (1989) *J. Bacteriol.* **171,** 6782–6790
4. Ramos, J. L., Mermod, N., and Timmis, K. N. (1987) *Mol. Microbiol.* **1,** 293–300
5. Inouye, S., Nakazawa, A., and Nakazawa, T. (1987) *Proc. Natl. Acad. Sci. U. S. A.* **84,** 5182–5186
6. Abril, M. A., Buck, M., and Ramos, J. L. (1991) *J. Biol. Chem.* **266,** 15832–15838
7. de Lorenzo, V., Herrero, M., Metzke, M., and Timmis, K. N. (1991) *EMBO. J.* **10,** 1159–1167
8. Buck, M., Cannon, W., and Woodcock, J. (1987) *Mol. Microbiol.* **1,** 243–249
9. Kustu, S., Santero, E., Keener, J., Popham, D., and Weiss, D. (1989) *Microbiol. Rev.* **53,** 367–376
10. Inouye, S., Gomada, M., Sangodkar, U. M. X., and Nakazawa, A. (1990) *J. Mol. Biol.* **216,** 251–260
11. Inouye, S., Nakazawa, A., and Nakazawa, T. (1988) *Gene (Amst.)* **66,** 301–306
12. Gross, R., Aricò, B., and Rappuoli, R. (1989) *Mol. Microbiol.* **3,** 1661–1667
13. Ninfa, A. J., and Magasanik, B. (1986) *Proc. Natl. Acad. Sci. U. S. A.* **83,** 5909–5913
14. Inouye, S., Nakazawa, A., and Nakazawa, T. (1983) *J. Bacteriol.* **155,** 1192–1199
15. Dixon, R. (1986) *Mol. Gen. Genet.* **203,** 129–136
16. Holtel, A., Timmis, K. N., and Ramos, J. L. (1992) *Nucleic Acids Res.* **20,** 1755–1762
17. Zoller, M. J., and Smith, M. (1983) *Methods Enzymol.* **100,** 468–500
18. Abril, M. A., and Ramos, J. L. (1993) *Mol. Gen. Genet.* **239,** 281–288
19. Ramos, J. L., Stolz, A., Reineke, W., and Timmis, K. N. (1986) *Proc. Natl. Acad. Sci. U. S. A.* **83,** 8467–8471
20. Marqués, S., Ramos, J. L., and Timmis, K. N. (1994) *Biochem. Biophys. Acta,* in press
21. Devereux, J., Haeberli, P., and Smithies, O. (1984) *Nucleic Acids Res.* **12,** 387–395
22. Needleman, S. B., and Wunsch, C. D. (1970) *J. Mol. Biol.* **48,** 443–453
23. Dayhoff, M. O. (1978) *Atlas of Protein Sequence and Structure* **5,** Suppl. 3, 1–8
24. Inouye, S., Nakazawa, A., and Nakazawa, T. (1984) *Proc. Natl. Acad. Sci. U. S. A.* **81,** 1688–1691
25. Franklin, F. C. H., Lehrbach, P. R., Lurz, R., Rueckert, B., Bagdasarian, M., and Timmis, K. N. (1983) *J. Bacteriol.* **154,** 676–685
26. Inouye, S., Nakazawa, A., and Nakazawa, T. (1981) *J. Bacteriol.* **148,** 413–418
27. North, A. K., Klose, K. E., Stedman, K. M., and Kustu, S. (1993) *J. Bacteriol.* **175,** 4267–4273
28. Shingler, V., Bartilson, M., and Moore, T. (1993) *J. Bacteriol.* **175,** 1596–1604
29. Wozniak, D. J., and Ohman, D. E. (1991) *J. Bacteriol.* **173,** 1406–1413
30. Ishimoto, K. S., and Lory, S. (1992) *J. Bacteriol.* **174,** 3514–3621
31. Ronson, C. W., Astwood, P. M., Nixon, B. J., and Ausubel, F. M. (1987) *Nucleic Acids Res.* **15,** 7921–7934
32. Ramakrishnan, G., and Newton, A. (1990) *Proc. Natl. Acad. Sci. U. S. A.* **87,** 2369–2373
33. Drummond, M., Whitty, P., and Wooton, J. (1986) *EMBO J.* **5,** 441–447
34. Joerger, R. D., Jacobson, M. R., and Bishop, P. E. (1989) *J. Bacteriol.* **171,** 3258–3267
35. Pittard, A. J., and Davison, B. E. (1991) *Mol. Microbiol.* **5,** 1585–1592
36. Weiss, V., and Magasanik, B. (1988) *Proc. Natl. Acad. Sci. U. S. A.* **85,** 8919–8923
37. Keener, J., and Kustu, S. (1988) *Proc. Natl. Acad. Sci. U. S. A.* **85,** 4976–4980
38. Frost, S., Delgado, J., and Inouye, M. (1989) *Proc. Natl. Acad. Sci. U. S. A.* **86,** 6052–6056
39. Egan, S. M., and Stewart, V. (1990) *J. Bacteriol.* **172,** 5020–5029
40. Harayama, S., and Timmis, K. N. (1989) in *Genetics of Bacterial Diversity* (Hopwood D. A., and Chater K. I., eds) pp. 154–174, Academic Press, London

[2] S. Marqués, A. Holtel, K. N. Timmis, and J. L. Ramos, submitted for publication.